

**IN THE CLAIMS:**

Claims 1-48 were previously cancelled. Claims 49-54 have been amended herein. All of the pending claims are presented below. This listing of claims will replace all prior versions and listings of claims in the application. Please enter these claims as amended.

**Listing of the Claims:**

1.-48. (Cancelled).

49. (Currently amended) A method for determining the prognosis for an AML affected subject, AML-affected subject, said method comprising the steps of:

- a) — determining, ~~by means of assays conducted on a substrate, in a sample obtained from the subject,~~ a level of expression of each of at least five cluster-specific genes selected from ~~one of the~~ a single cluster selected from the group consisting of clusters #9, #12, and #13, corresponding to AML classes of inv(16), t(15; 17) or t(8;21) respectively;
- b) — establishing the similarity ~~of the level of expression of said~~ between the at least five cluster-specific genes in ~~said the AML-affected subject to the level of the expression of~~ said and the at least five cluster-specific genes in patients selected from ~~an established~~ the corresponding AML class ~~selected from the group consisting of inv(16), t(15; 17) and t(8;21)~~; and
- c) — assigning to ~~said the AML-affected subject~~ a prognosis based on the ~~established level of expression~~ similarity level of the expression of step e) ~~between the~~ at least five cluster-specific genes in said the AML-affected subject corresponding to the established and the at least five cluster-specific genes in patients selected from the corresponding AML class.

50. (Currently amended) The method according to ~~claim 49~~ claim 49, wherein ~~in step e)~~ ~~the substrate is an Affymetrix GeneChip determining the level of expression is performed with a gene chip~~.

51. (Currently amended) The method according to ~~claim 50~~ claim 49, wherein ~~in step~~  
a) the level of expression of each of at least eight cluster-specific genes is determined.

52. (Currently amended) ~~Method~~ The method according to ~~claim 50~~ claim 49,  
wherein the at least five cluster-specific genes from a single cluster ~~cluster #9~~ are MYH11,  
CLIPR-59, ST18, NRP1 and CLECSF13 from cluster #9.

53. (Currently amended) ~~Method~~ The method according to ~~claim 50~~ claim 49,  
wherein the at least five cluster-specific genes from a single cluster ~~cluster #12~~ are HGF, FGF13,  
MEG3, GABRE and MST1 from cluster #12.

54. (Currently amended) ~~Method~~ The method according to ~~claim 50~~ claim 49,  
wherein the at least five cluster-specific genes from a single cluster ~~cluster #13~~ are CBFA2T1,  
ROBO1, CACNA2D2, POU4F1 and IL5RA from cluster #13.